Please also amend the specification by deleting Sequence Submission pp. 84-110, and substitute therefore the attached Sequence Submission, pp. 84-108.

REMARKS

The amendments to the related application section provide the filing dates for the individual priority applications from which this application claims benefit.

The amendments to the sequence listing correct various formalities in the originally filed listing of the parent application. No new matter is added thereby.

The Applicants also attach a request under 37 C.F.R. § 1.821(e) that the computer-readable form filed in the parent Application No. 09/351,777 be used as the computer-readable form for the instant application.

I hereby state that the informational contents of the paper and computer readable copies of the above Sequence Listing are believed to be the same. This submission involves no new matter as the enclosed sequences are the same as those filed in the priority documents.

CONCLUSION

If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 415-576-0200.

Respectfully submitted,

Frank J. Mycroft
Reg. No. 46,946

TOWNSEND and TOWNSEND and CREW LLP
Two Embarcadero Center, 8th Floor
San Francisco, California 94111-3834
Tel: (415) 576-0200
Fax: (415) 576-0300
FJM:meg
SF 1215778 v1

VERSION WITH MARKINGS TO SHOW CHANGES

In the Specification:

This application is a Continuation Application of U.S. Patent Utility Application No. 09/351,777 filed on July 12, 1999. USSN 09/351,777 was a conversion to a U.S. Utility Patent Application of U.S. Provisional Patent Application of USSN 60/092,658 which was filed on July 13, 1998; USSN 60/093,897 which was filed on July 23, 1998; and USSN 60/099,999 which was filed on September 11, 1998. This application incorporates herein by reference, and claims priority to, each of these four applications. [This filing is a conversion to a U.S. Utility Patent Application of U.S. Provisional Patent Applications USSN 60/092,658; USSN 60/093,897; and USSN 60/099,999; each of which is incorporated herein by reference].

SEQUENCE SUBMISSION

Sub A2

SEQ ID NO: 1 is a primate HDTEA84 nucleic acid sequence.
SEQ ID NO: 2 is a primate HDTEA84 amino acid sequence.
SEQ ID NO: 3 is a primate HSLJD37R nucleic acid sequence.
SEQ ID NO: 4 is a primate HSLJD37R amino acid sequence.
SEQ ID NO: 5 is supplemented primate HSLJD37R nucleic acid sequence.
SEQ ID NO: 6 is supplemented primate HSLJD37R amino acid sequence.
SEQ ID NO: 7 is variant primate HSLJD37R nucleic acid sequence.
SEQ ID NO: 8 is variant primate HSLJD37R amino acid sequence.
SEQ ID NO: 9 is murine TNF-R2 amino acid sequence.
SEQ ID NO: 10 is human TNF-R2 amino acid sequence.
SEQ ID NO: 11 is human OPG amino acid sequence.
SEQ ID NO: 12 is a rodent RANKL nucleic acid sequence.
SEQ ID NO: 13 is a rodent RANKL amino acid sequence.
SEQ ID NO: 14 is a primate RANKL nucleic acid sequence.
SEQ ID NO: 15 is a primate RANKL amino acid sequence.
SEQ ID NO: 16 is another primate RANKL nucleic acid sequence.
SEQ ID NO: 17 is another primate RANKL amino acid sequence.
SEQ ID NO: 18 is a variant primate RANKL nucleic acid sequence.
SEQ ID NO: 19 is a variant primate RANKL amino acid sequence.

<110> Murphy, Erin E.
Mattson, Jeanine D.
Bates, Elizabeth Esther Mary
Gorman, Daniel M.
Lebecque, Serge J.E.

<120> Mammalian Genes; Related Reagents

<130> SF0818K

<140>
<141>

<160> 19

<170> PatentIn Ver. 2.0

<210> 1
<211> 1137
<212> DNA
<213> primate

<220>
<221> CDS
<222> (99)..(998)

<220>
<221> misc_feature
<222> (367)
<223> W; may be A or T; translated amino acid depends on genetic code

<220>
<221> mat_peptide
<222> (132)..(998)

<400> 1
cgcaggcgga ccgggggcaa aggaggtggc atgtcggtca ggcacagcag ggtcctgtgt 60

SubA2

```
ccgcgctgag ccgcgctctc cctgctccag caaggacc atg agg gcg ctg gag ggg 116
                                          Met Arg Ala Leu Glu Gly
                                              -10

cca ggc ctg tcg ctg ctg tgc ctg gtg ttg gcg ctg cct gcc ctg ctg   164
Pro Gly Leu Ser Leu Leu Cys Leu Val Leu Ala Leu Pro Ala Leu Leu
 -5              -1   1               5                  10

ccg gtg ccg gct gta cgc gga gtg gca gaa aca ccc acc tac ccc tgg   212
Pro Val Pro Ala Val Arg Gly Val Ala Glu Thr Pro Thr Tyr Pro Trp
            15                  20                  25

cgg gac gca gag aca ggg gag cgg ctg gtg tgc gcc cag tgc ccc cca   260
Arg Asp Ala Glu Thr Gly Glu Arg Leu Val Cys Ala Gln Cys Pro Pro
        30                  35                  40

ggc acc ttt gtg cag cgg ccg tgc cgc cga gac agc ccc atg acg tgt   308
Gly Thr Phe Val Gln Arg Pro Cys Arg Arg Asp Ser Pro Met Thr Cys
    45                  50                  55

ggc ccg tgt cca ccg cgc cac tac acg cag ttc tgg aac tac ctg gag   356
Gly Pro Cys Pro Pro Arg His Tyr Thr Gln Phe Trp Asn Tyr Leu Glu
60                  65                  70                  75

cgc tgc cgc twc tgc tac gtc ctc tgc ggg gag cgt gag gag gag gca   404
Arg Cys Arg Xaa Cys Tyr Val Leu Cys Gly Glu Arg Glu Glu Glu Ala
                80                  85                  90

cgg gct tgc cac gcc acc cac aac cgt gcc tgc cgc tgc cgc acc ggc   452
Arg Ala Cys His Ala Thr His Asn Arg Ala Cys Arg Cys Arg Thr Gly
            95                  100                 105

ttc ttc gcg cac gct ggt ttc tgc ttg gag cac gca tcg tgt cca cct   500
Phe Phe Ala His Ala Gly Phe Cys Leu Glu His Ala Ser Cys Pro Pro
        110                 115                 120

ggt gcc ggc gtg att gcc ccg ggc acc ccc agc cag aac acg cag tgc   548
Gly Ala Gly Val Ile Ala Pro Gly Thr Pro Ser Gln Asn Thr Gln Cys
    125                 130                 135

cag ccg tgc ccc cca ggc acc ttc tca gcc agc agc tcc agc tca gag   596
Gln Pro Cys Pro Pro Gly Thr Phe Ser Ala Ser Ser Ser Ser Ser Glu
140                 145                 150                 155

cag tgc cag ccc cac cgc aac tgc acg gcc ctg ggc ctg gcc ctc aat   644
Gln Cys Gln Pro His Arg Asn Cys Thr Ala Leu Gly Leu Ala Leu Asn
                160                 165                 170

gtg cca ggc tct tcc tcc cat gac acc ctg tgc acc agc tgc act ggc   692
Val Pro Gly Ser Ser Ser His Asp Thr Leu Cys Thr Ser Cys Thr Gly
            175                 180                 185

ttc ccc ctc agc acc agg gta cca gga gct gag gag tgt gag cgt gcc   740
Phe Pro Leu Ser Thr Arg Val Pro Gly Ala Glu Glu Cys Glu Arg Ala
        190                 195                 200

gtc atc gac ttt gtg gct ttc cag gac atc tcc atc aag agg ctg cag   788
Val Ile Asp Phe Val Ala Phe Gln Asp Ile Ser Ile Lys Arg Leu Gln
    205                 210                 215
```

SubA2

cgg ctg ctg cag gcc ctc gag gcc ccg gag ggc tgg ggt ccg aca cca 836
Arg Leu Leu Gln Ala Leu Glu Ala Pro Glu Gly Trp Gly Pro Thr Pro
220 225 230 235

agg gcg ggc cgc gcg gcc ttg cag ctg aag ctg cgt cgg cgg ctc acg 884
Arg Ala Gly Arg Ala Ala Leu Gln Leu Lys Leu Arg Arg Arg Leu Thr
240 245 250

gag ctc ctg ggg gcg cag gac ggg gcg ctg ctg gtg cgg ctg ctg cag 932
Glu Leu Leu Gly Ala Gln Asp Gly Ala Leu Leu Val Arg Leu Leu Gln
255 260 265

gcg ctg cgc gtg gcc agg atg ccc ggg ctg gag cgg agc gtc cgt gag 980
Ala Leu Arg Val Ala Arg Met Pro Gly Leu Glu Arg Ser Val Arg Glu
270 275 280

cgc ttc ctc cct gtg cac tgatcctggc cccctcttat ttattctaca 1028
Arg Phe Leu Pro Val His
285

tccttggcac cccacttgca ctgaaagagg ctttttttta aatagaagaa atgaggtttc 1088

ttaaagctta tttttataaa gctttttcat aaaaaaaaaa aaaaaaaaa 1137

<210> 2
<211> 300
<212> PRT
<213> primate

<400> 2
Met Arg Ala Leu Glu Gly Pro Gly Leu Ser Leu Leu Cys Leu Val Leu
-10 -5 -1 1 5

Ala Leu Pro Ala Leu Leu Pro Val Pro Ala Val Arg Gly Val Ala Glu
10 15 20

Thr Pro Thr Tyr Pro Trp Arg Asp Ala Glu Thr Gly Glu Arg Leu Val
25 30 35

Cys Ala Gln Cys Pro Pro Gly Thr Phe Val Gln Arg Pro Cys Arg Arg
40 45 50

Asp Ser Pro Met Thr Cys Gly Pro Cys Pro Pro Arg His Tyr Thr Gln
55 60 65

Phe Trp Asn Tyr Leu Glu Arg Cys Arg Xaa Cys Tyr Val Leu Cys Gly
70 75 80 85

Glu Arg Glu Glu Glu Ala Arg Ala Cys His Ala Thr His Asn Arg Ala
90 95 100

Cys Arg Cys Arg Thr Gly Phe Phe Ala His Ala Gly Phe Cys Leu Glu
105 110 115

His Ala Ser Cys Pro Pro Gly Ala Gly Val Ile Ala Pro Gly Thr Pro
120 125 130

Ser Gln Asn Thr Gln Cys Gln Pro Cys Pro Pro Gly Thr Phe Ser Ala

Sub A2

135 140 145

Ser Ser Ser Ser Ser Glu Gln Cys Gln Pro His Arg Asn Cys Thr Ala
150 155 160 165

Leu Gly Leu Ala Leu Asn Val Pro Gly Ser Ser Ser His Asp Thr Leu
170 175 180

Cys Thr Ser Cys Thr Gly Phe Pro Leu Ser Thr Arg Val Pro Gly Ala
185 190 195

Glu Glu Cys Glu Arg Ala Val Ile Asp Phe Val Ala Phe Gln Asp Ile
200 205 210

Ser Ile Lys Arg Leu Gln Arg Leu Leu Gln Ala Leu Glu Ala Pro Glu
215 220 225

Gly Trp Gly Pro Thr Pro Arg Ala Gly Arg Ala Ala Leu Gln Leu Lys
230 235 240 245

Leu Arg Arg Arg Leu Thr Glu Leu Leu Gly Ala Gln Asp Gly Ala Leu
250 255 260

Leu Val Arg Leu Leu Gln Ala Leu Arg Val Ala Arg Met Pro Gly Leu
265 270 275

Glu Arg Ser Val Arg Glu Arg Phe Leu Pro Val His
280 285

<210> 3
<211> 1031
<212> DNA
<213> primate

<220>
<221> CDS
<222> (402)..(1031)

<220>
<221> mat_peptide
<222> (525)..(1031)

<220>
<221> misc_feature
<222> (2)
<223> N at 2 or 9; may be A, C, G, or T

<220>
<221> misc_feature
<222> (664)
<223> K; may be G or T; translated amino acid depends on genetic code

<220>
<221> misc_feature
<222> (956)
<223> N at 956 and 8989 may be A, C, G, or T; translated amino acid depends on genetic code

Sub A2

<400> 3

```
cngactcant ccctcgccga ccagtctggg cagcggagga gggtggttgg cagtggctgg 60

aagcttcgct atgggaagtc gttcctttgc tctctcgcgc ccagtcctcc tccctggttc 120

tcctcagccg ctgtcggagg agagcacccg gagacgcggg ctgcagtcgc ggcggcttct 180

ccccgcctgg gcggccgcgc cgctgggcag gtgctgagcg cccctagagc ctcccttgcc 240

gcctccctcc tctgcccggc cgcagcagtg cacatggggt gttggaggta gatgggctcc 300

cggcccggga ggcggcggtg gatgcggcgc tgggcagaag cagccgccga ttccagctgc 360

cccgcgcgcc ccgggcgccc ctgcgagtcc ccggttcagc c atg ggg acc tct ccg 416
                                                Met Gly Thr Ser Pro
                                                     -40

agc agc agc acc gcc ctc gcc tcc tgc agc cgc atc gcc cgc cga gcc   464
Ser Ser Ser Thr Ala Leu Ala Ser Cys Ser Arg Ile Ala Arg Arg Ala
   -35                 -30                 -25

aca gcc acg atg atc gcg ggc tcc ctt ctc ctg ctt gga ttc ctt agc   512
Thr Ala Thr Met Ile Ala Gly Ser Leu Leu Leu Leu Gly Phe Leu Ser
-20                 -15                 -10                  -5

acc acc aca gct cag cca gaa cag aag gcc tcg aat ctc att ggc aca   560
Thr Thr Thr Ala Gln Pro Glu Gln Lys Ala Ser Asn Leu Ile Gly Thr
             -1   1                   5                  10

tac cgc cat gtt gac cgt gcc acc ggc cag gtg cta acc tgt gac aag   608
Tyr Arg His Val Asp Arg Ala Thr Gly Gln Val Leu Thr Cys Asp Lys
         15                  20                  25

tgt cca gca gga acc tat gtc tct gag cat tgt acc aac aca agc tgc   656
Cys Pro Ala Gly Thr Tyr Val Ser Glu His Cys Thr Asn Thr Ser Cys
     30                  35                  40

gcg tct gkc agc agt tgc cct gtg ggg acc ttt acc agg cat gag aat   704
Ala Ser Xaa Ser Ser Cys Pro Val Gly Thr Phe Thr Arg His Glu Asn
 45                  50                  55                  60

ggc ata gag aaa tgc cat gac tgt agt cag cca tgc cca tgg cca atg   752
Gly Ile Glu Lys Cys His Asp Cys Ser Gln Pro Cys Pro Trp Pro Met
                 65                  70                  75

att gag aaa tta cct tgt gct gcc ttg act gac cga gaa tgc act tgc   800
Ile Glu Lys Leu Pro Cys Ala Ala Leu Thr Asp Arg Glu Cys Thr Cys
             80                  85                  90

cca cct ggc atg ttc cag tct aac gct acc tgt gcc ccc cat acg gtg   848
Pro Pro Gly Met Phe Gln Ser Asn Ala Thr Cys Ala Pro His Thr Val
         95                  100                 105

tgt cct gtg ggt tgg ggt gtg cgg aag aaa ggg aca gag act gag gat   896
Cys Pro Val Gly Trp Gly Val Arg Lys Lys Gly Thr Glu Thr Glu Asp
    110                 115                 120

gtg cgg tgt aag cag tgt gct cgg ggg tac ttc tca gat gtg cct tct   944
Val Arg Cys Lys Gln Cys Ala Arg Gly Tyr Phe Ser Asp Val Pro Ser
125                 130                 135                 140
```

agt gtg atg aan gca aag cat aca cag act gtc tgg atc aga acn tgg 992
Ser Val Met Xaa Ala Lys His Thr Gln Thr Val Trp Ile Arg Xaa Trp
145 150 155

ttg gtg atc aag ccg ggg gga cca agg aga cag aca act 1031
Leu Val Ile Lys Pro Gly Gly Pro Arg Arg Gln Thr Thr
160 165

<210> 4
<211> 210
<212> PRT
<213> primate

<400> 4
Met Gly Thr Ser Pro Ser Ser Ser Thr Ala Leu Ala Ser Cys Ser Arg
-40 -35 -30

Ile Ala Arg Arg Ala Thr Ala Thr Met Ile Ala Gly Ser Leu Leu Leu
-25 -20 -15 -10

Leu Gly Phe Leu Ser Thr Thr Thr Ala Gln Pro Glu Gln Lys Ala Ser
-5 -1 1 5

Asn Leu Ile Gly Thr Tyr Arg His Val Asp Arg Ala Thr Gly Gln Val
10 15 20

Leu Thr Cys Asp Lys Cys Pro Ala Gly Thr Tyr Val Ser Glu His Cys
25 30 35

Thr Asn Thr Ser Cys Ala Ser Xaa Ser Ser Cys Pro Val Gly Thr Phe
40 45 50 55

Thr Arg His Glu Asn Gly Ile Glu Lys Cys His Asp Cys Ser Gln Pro
60 65 70

Cys Pro Trp Pro Met Ile Glu Lys Leu Pro Cys Ala Ala Leu Thr Asp
75 80 85

Arg Glu Cys Thr Cys Pro Pro Gly Met Phe Gln Ser Asn Ala Thr Cys
90 95 100

Ala Pro His Thr Val Cys Pro Val Gly Trp Gly Val Arg Lys Lys Gly
105 110 115

Thr Glu Thr Glu Asp Val Arg Cys Lys Gln Cys Ala Arg Gly Tyr Phe
120 125 130 135

Ser Asp Val Pro Ser Ser Val Met Xaa Ala Lys His Thr Gln Thr Val
140 145 150

Trp Ile Arg Xaa Trp Leu Val Ile Lys Pro Gly Gly Pro Arg Arg Gln
155 160 165

Thr Thr

<210> 5

<211> 2877
<212> DNA
<213> primate

<220>
<221> CDS
<222> (410)..(2374)

<220>
<221> mat_peptide
<222> (533)..(2374)

<400> 5
ggcacgagcc gactcagtcc ctcgccgacc agtctgggca gcggaggagg gtggttggca 60

gtggctggaa gcttcgctat gggaagtcgt tcctttgctc tctcgcgccc agtcctcctc 120

cctggttctc ctcagccgct gtcggaggag agcacccgga gacgcgggct gcagtcgcgg 180

cggcttctcc ccgcctgggc ggccgcgccg ctgggcaggt gctgagcgcc cctagcgcct 240

cccttgccgc ctccctcctc tgcccggccg cagcagtgca catggggtgt tggaggtaga 300

tgggctcccg gcccgggagg cggcggtgga tgcggcgctg ggcagaagca gccgccgatt 360

ccagctgccc cgcgcgcccc gggcgccccc gcgagtcccc ggttcagcc atg ggg acc 418
Met Gly Thr
-40

tct ccg agc agc agc acc gcc ctc gcc tcc tgc agc cgc atc gcc cgc 466
Ser Pro Ser Ser Ser Thr Ala Leu Ala Ser Cys Ser Arg Ile Ala Arg
-35 -30 -25

cga gcc aca gcc acg atg atc gcg ggc tcc ctt ctc ctg ctt gga ttc 514
Arg Ala Thr Ala Thr Met Ile Ala Gly Ser Leu Leu Leu Leu Gly Phe
-20 -15 -10

ctt agc acc acc aca gct cag cca gaa cag aag gcc tcg aat ctc att 562
Leu Ser Thr Thr Thr Ala Gln Pro Glu Gln Lys Ala Ser Asn Leu Ile
-5 -1 1 5 10

ggc aca tac cgc cat gtt gac cgt gcc acc ggc cag gtg cta acc tgt 610
Gly Thr Tyr Arg His Val Asp Arg Ala Thr Gly Gln Val Leu Thr Cys
15 20 25

gac aag tgt cca gca gga acc tat gtc tct gag cat tgt acc aac aca 658
Asp Lys Cys Pro Ala Gly Thr Tyr Val Ser Glu His Cys Thr Asn Thr
30 35 40

agc ctg cgc gtc tgc agc agt tgc cct gtg ggg acc ttt acc agg cat 706
Ser Leu Arg Val Cys Ser Ser Cys Pro Val Gly Thr Phe Thr Arg His
45 50 55

gag aat ggc ata gag aaa tgc cat gac tgt agt cag cca tgc cca tgg 754
Glu Asn Gly Ile Glu Lys Cys His Asp Cys Ser Gln Pro Cys Pro Trp
60 65 70

cca atg att gag aaa tta cct tgt gct gcc ttg act gac cga gaa tgc 802
Pro Met Ile Glu Lys Leu Pro Cys Ala Ala Leu Thr Asp Arg Glu Cys
75 80 85 90

Sub A2

```
act tgc cca cct ggc atg ttc cag tct aac gct acc tgt gcc ccc cat    850
Thr Cys Pro Pro Gly Met Phe Gln Ser Asn Ala Thr Cys Ala Pro His
                95                  100                 105

acg gtg tgt cct gtg ggt tgg ggt gtg cgg aag aaa ggg aca gag act    898
Thr Val Cys Pro Val Gly Trp Gly Val Arg Lys Lys Gly Thr Glu Thr
            110                 115                 120

gag gat gtg cgg tgt aag cag tgt gct cgg ggt acc ttc tca gat gtg    946
Glu Asp Val Arg Cys Lys Gln Cys Ala Arg Gly Thr Phe Ser Asp Val
        125                 130                 135

cct tct agt gtg atg aaa tgc aaa gca tac aca gac tgt ctg agt cag    994
Pro Ser Ser Val Met Lys Cys Lys Ala Tyr Thr Asp Cys Leu Ser Gln
    140                 145                 150

aac ctg gtg gtg atc aag ccg ggg acc aag gag aca gac aac gtc tgt   1042
Asn Leu Val Val Ile Lys Pro Gly Thr Lys Glu Thr Asp Asn Val Cys
155                 160                 165                 170

ggc aca ctc ccg tcc ttc tcc agc tcc acc tca cct tcc cct ggc aca   1090
Gly Thr Leu Pro Ser Phe Ser Ser Ser Thr Ser Pro Ser Pro Gly Thr
                175                 180                 185

gcc atc ttt cca cgc cct gag cac atg gaa acc cat gaa gtc cct tcc   1138
Ala Ile Phe Pro Arg Pro Glu His Met Glu Thr His Glu Val Pro Ser
            190                 195                 200

tcc act tat gtt ccc aaa ggc atg aac tca aca gaa tcc aac tct tct   1186
Ser Thr Tyr Val Pro Lys Gly Met Asn Ser Thr Glu Ser Asn Ser Ser
        205                 210                 215

gcc tct gtt aga cca aag gta ctg agt agc atc cag gaa ggg aca gtc   1234
Ala Ser Val Arg Pro Lys Val Leu Ser Ser Ile Gln Glu Gly Thr Val
    220                 225                 230

cct gac aac aca agc tca gca agg ggg aag gaa gac gtg aac aag acc   1282
Pro Asp Asn Thr Ser Ser Ala Arg Gly Lys Glu Asp Val Asn Lys Thr
235                 240                 245                 250

ctc cca aac ctt cag gta gtc aac cac cag caa ggc ccc cac cac aga   1330
Leu Pro Asn Leu Gln Val Val Asn His Gln Gln Gly Pro His His Arg
                255                 260                 265

cac atc ctg aag ctg ctg ccg tcc atg gag gcc act ggg ggc gag aag   1378
His Ile Leu Lys Leu Leu Pro Ser Met Glu Ala Thr Gly Gly Glu Lys
            270                 275                 280

tcc agc acg ccc atc aag ggc ccc aag agg gga cat cct aga cag aac   1426
Ser Ser Thr Pro Ile Lys Gly Pro Lys Arg Gly His Pro Arg Gln Asn
        285                 290                 295

cta cac aag cat ttt gac atc aat gag cat ttg ccc tgg atg att gtg   1474
Leu His Lys His Phe Asp Ile Asn Glu His Leu Pro Trp Met Ile Val
    300                 305                 310

ctt ttc ctg ctg ctg gtg ctt gtg gtg att gtg gtg tgc agt atc cgg   1522
Leu Phe Leu Leu Leu Val Leu Val Val Ile Val Val Cys Ser Ile Arg
315                 320                 325                 330
```

```
aaa agc tcg agg act ctg aaa aag ggg ccc cgg cag gat ccc agt gcc   1570
Lys Ser Ser Arg Thr Leu Lys Lys Gly Pro Arg Gln Asp Pro Ser Ala
                335                 340                 345

att gtg gaa aag gca ggg ctg aag aaa tcc atg act cca acc cag aac   1618
Ile Val Glu Lys Ala Gly Leu Lys Lys Ser Met Thr Pro Thr Gln Asn
            350                 355                 360

cgg gag aaa tgg atc tac tac tgc aat ggc cat ggt atc gat atc ctg   1666
Arg Glu Lys Trp Ile Tyr Tyr Cys Asn Gly His Gly Ile Asp Ile Leu
        365                 370                 375

aag ctt gta gca gcc caa gtg gga agc cag tgg aaa gat atc tat cag   1714
Lys Leu Val Ala Ala Gln Val Gly Ser Gln Trp Lys Asp Ile Tyr Gln
    380                 385                 390

ttt ctt tgc aat gcc agt gag agg gag gtt gct gct ttc tcc aat ggg   1762
Phe Leu Cys Asn Ala Ser Glu Arg Glu Val Ala Ala Phe Ser Asn Gly
395                 400                 405                 410

tac aca gcc gac cac gag cgg gcc tac gca gct ctg cag cac tgg acc   1810
Tyr Thr Ala Asp His Glu Arg Ala Tyr Ala Ala Leu Gln His Trp Thr
                415                 420                 425

atc cgg ggc ccc gag gcc agc ctc gcc cag cta att agc gcc ctg cgc   1858
Ile Arg Gly Pro Glu Ala Ser Leu Ala Gln Leu Ile Ser Ala Leu Arg
            430                 435                 440

cag cac cgg aga aac gat gtt gtg gag aag att cgt ggg ctg atg gaa   1906
Gln His Arg Arg Asn Asp Val Val Glu Lys Ile Arg Gly Leu Met Glu
        445                 450                 455

gac acc acc cag ctg gaa act gac aaa cta gct ctc ccg atg agc ccc   1954
Asp Thr Thr Gln Leu Glu Thr Asp Lys Leu Ala Leu Pro Met Ser Pro
    460                 465                 470

agc ccg ctt agc ccg agc ccc atc ccc agc ccc aac gcg aaa ctt gag   2002
Ser Pro Leu Ser Pro Ser Pro Ile Pro Ser Pro Asn Ala Lys Leu Glu
475                 480                 485                 490

aat tcc gct ctc ctg acg gtg gag cct tcc cca cag gac aag aac aag   2050
Asn Ser Ala Leu Leu Thr Val Glu Pro Ser Pro Gln Asp Lys Asn Lys
                495                 500                 505

ggc ttc ttc gtg gat gag tcg gag ccc ctt ctc cgc tgt gac tct aca   2098
Gly Phe Phe Val Asp Glu Ser Glu Pro Leu Leu Arg Cys Asp Ser Thr
            510                 515                 520

tcc agc ggc tcc tcc gcg ctg agc agg aac ggt tcc ttt att acc aaa   2146
Ser Ser Gly Ser Ser Ala Leu Ser Arg Asn Gly Ser Phe Ile Thr Lys
        525                 530                 535

gaa aag aag gac aca gtg ttg cgg cag gta cgc ctg gac ccc tgt gac   2194
Glu Lys Lys Asp Thr Val Leu Arg Gln Val Arg Leu Asp Pro Cys Asp
    540                 545                 550

ttg cag cct atc ttt gat gac atg ctc cac ttt cta aat cct gag gag   2242
Leu Gln Pro Ile Phe Asp Asp Met Leu His Phe Leu Asn Pro Glu Glu
555                 560                 565                 570
```

ctg cgg gtg att gaa gag att ccc cag gct gag gac aaa cta gac cgg 2290
Leu Arg Val Ile Glu Glu Ile Pro Gln Ala Glu Asp Lys Leu Asp Arg
575 580 585

cta ttc gaa att att gga gtc aag agc cag gaa gcc agc cag acc ctc 2338
Leu Phe Glu Ile Ile Gly Val Lys Ser Gln Glu Ala Ser Gln Thr Leu
590 595 600

ctg gac tct gtt tat agc cat ctt cct gac ctg ctg tagaacatag 2384
Leu Asp Ser Val Tyr Ser His Leu Pro Asp Leu Leu
605 610

ggatactgca ttctggaaat tactcaattt agtggcaggg tggtttttta atttccttct 2444

gtgtctgatt tttgttgttt ggggtgtgtg tgtgtgtttg tgtgtgtgtg tgtgtgtgtg 2504

tgtgtgtgtg tttaacagag aatatggcca gtgcttgagt tctttctcct tctctctctc 2564

tctttttttt ttaaataact cttctgggaa gttggtttat aagcctttgc caggtgtaac 2624

tgttgtgaaa tacccaccac taaagttttt taagttccat attttctcca ttttgccttc 2684

ttatgtattt tcaagattat tctgtgcact ttaaatttac tcaacttacc ataaatgcag 2744

tgtgactttt cccacacact ggattgtgag gctcttaact tcttaaaagt ataatggcat 2804

cttgtgaatc ctataagcag tctttatgtc tcttaacatt cacacctact ttttaaaaac 2864

aaatattatt act 2877

<210> 6
<211> 655
<212> PRT
<213> primate

<400> 6
Met Gly Thr Ser Pro Ser Ser Ser Thr Ala Leu Ala Ser Cys Ser Arg
-40 -35 -30

Ile Ala Arg Arg Ala Thr Ala Thr Met Ile Ala Gly Ser Leu Leu Leu
-25 -20 -15 -10

Leu Gly Phe Leu Ser Thr Thr Thr Ala Gln Pro Glu Gln Lys Ala Ser
-5 -1 1 5

Asn Leu Ile Gly Thr Tyr Arg His Val Asp Arg Ala Thr Gly Gln Val
10 15 20

Leu Thr Cys Asp Lys Cys Pro Ala Gly Thr Tyr Val Ser Glu His Cys
25 30 35

Thr Asn Thr Ser Leu Arg Val Cys Ser Ser Cys Pro Val Gly Thr Phe
40 45 50 55

Thr Arg His Glu Asn Gly Ile Glu Lys Cys His Asp Cys Ser Gln Pro
60 65 70

Cys Pro Trp Pro Met Ile Glu Lys Leu Pro Cys Ala Ala Leu Thr Asp

75 80 85

Arg Glu Cys Thr Cys Pro Pro Gly Met Phe Gln Ser Asn Ala Thr Cys
90 95 100

Ala Pro His Thr Val Cys Pro Val Gly Trp Gly Val Arg Lys Lys Gly
105 110 115

Thr Glu Thr Glu Asp Val Arg Cys Lys Gln Cys Ala Arg Gly Thr Phe
120 125 130 135

Ser Asp Val Pro Ser Ser Val Met Lys Cys Lys Ala Tyr Thr Asp Cys
140 145 150

Leu Ser Gln Asn Leu Val Val Ile Lys Pro Gly Thr Lys Glu Thr Asp
155 160 165

Asn Val Cys Gly Thr Leu Pro Ser Phe Ser Ser Ser Thr Ser Pro Ser
170 175 180

Pro Gly Thr Ala Ile Phe Pro Arg Pro Glu His Met Glu Thr His Glu
185 190 195

Val Pro Ser Ser Thr Tyr Val Pro Lys Gly Met Asn Ser Thr Glu Ser
200 205 210 215

Asn Ser Ser Ala Ser Val Arg Pro Lys Val Leu Ser Ser Ile Gln Glu
220 225 230

Gly Thr Val Pro Asp Asn Thr Ser Ser Ala Arg Gly Lys Glu Asp Val
235 240 245

Asn Lys Thr Leu Pro Asn Leu Gln Val Val Asn His Gln Gln Gly Pro
250 255 260

His His Arg His Ile Leu Lys Leu Leu Pro Ser Met Glu Ala Thr Gly
265 270 275

Gly Glu Lys Ser Ser Thr Pro Ile Lys Gly Pro Lys Arg Gly His Pro
280 285 290 295

Arg Gln Asn Leu His Lys His Phe Asp Ile Asn Glu His Leu Pro Trp
300 305 310

Met Ile Val Leu Phe Leu Leu Leu Val Leu Val Val Ile Val Val Cys
315 320 325

Ser Ile Arg Lys Ser Ser Arg Thr Leu Lys Lys Gly Pro Arg Gln Asp
330 335 340

Pro Ser Ala Ile Val Glu Lys Ala Gly Leu Lys Lys Ser Met Thr Pro
345 350 355

Thr Gln Asn Arg Glu Lys Trp Ile Tyr Tyr Cys Asn Gly His Gly Ile
360 365 370 375

Asp Ile Leu Lys Leu Val Ala Ala Gln Val Gly Ser Gln Trp Lys Asp
380 385 390

Ile Tyr Gln Phe Leu Cys Asn Ala Ser Glu Arg Glu Val Ala Ala Phe

395 400 405

Ser Asn Gly Tyr Thr Ala Asp His Glu Arg Ala Tyr Ala Ala Leu Gln
410 415 420

His Trp Thr Ile Arg Gly Pro Glu Ala Ser Leu Ala Gln Leu Ile Ser
425 430 435

Ala Leu Arg Gln His Arg Arg Asn Asp Val Val Glu Lys Ile Arg Gly
440 445 450 455

Leu Met Glu Asp Thr Thr Gln Leu Glu Thr Asp Lys Leu Ala Leu Pro
460 465 470

Met Ser Pro Ser Pro Leu Ser Pro Ser Pro Ile Pro Ser Pro Asn Ala
475 480 485

Lys Leu Glu Asn Ser Ala Leu Leu Thr Val Glu Pro Ser Pro Gln Asp
490 495 500

Lys Asn Lys Gly Phe Phe Val Asp Glu Ser Glu Pro Leu Leu Arg Cys
505 510 515

Asp Ser Thr Ser Ser Gly Ser Ser Ala Leu Ser Arg Asn Gly Ser Phe
520 525 530 535

Ile Thr Lys Glu Lys Lys Asp Thr Val Leu Arg Gln Val Arg Leu Asp
540 545 550

Pro Cys Asp Leu Gln Pro Ile Phe Asp Asp Met Leu His Phe Leu Asn
555 560 565

Pro Glu Glu Leu Arg Val Ile Glu Glu Ile Pro Gln Ala Glu Asp Lys
570 575 580

Leu Asp Arg Leu Phe Glu Ile Ile Gly Val Lys Ser Gln Glu Ala Ser
585 590 595

Gln Thr Leu Leu Asp Ser Val Tyr Ser His Leu Pro Asp Leu Leu
600 605 610

<210> 7
<211> 1474
<212> DNA
<213> primate

<220>
<221> CDS
<222> (1)..(1332)

<220>
<221> mat_peptide
<222> (124)..(1332)

<400> 7
atg ggg acc tct ccg agc agc agc acc gcc ctc gcc tcc tgc agc cgc 48
Met Gly Thr Ser Pro Ser Ser Ser Thr Ala Leu Ala Ser Cys Ser Arg
-40 -35 -30

```
atc gcc cgc cga gcc aca gcc acg atg atc gcg ggc tcc ctt ctc ctg    96
Ile Ala Arg Arg Ala Thr Ala Thr Met Ile Ala Gly Ser Leu Leu Leu
-25                 -20                 -15                 -10

ctt gga ttc ctt agc acc acc aca gct cag cca gaa cag aag gcc tcg   144
Leu Gly Phe Leu Ser Thr Thr Thr Ala Gln Pro Glu Gln Lys Ala Ser
                -5                  -1   1                   5

aat ctc att ggc aca tac cgc cat gtt gac cgt gcc acc ggc cag gtg   192
Asn Leu Ile Gly Thr Tyr Arg His Val Asp Arg Ala Thr Gly Gln Val
          10                  15                  20

cta acc tgt gac aag tgt cca gca gga acc tat gtc tct gag cat tgt   240
Leu Thr Cys Asp Lys Cys Pro Ala Gly Thr Tyr Val Ser Glu His Cys
     25                  30                  35

acc aac aca agc ctg cgc gtc tgc agc agt tgc cct gtg ggg acc ttt   288
Thr Asn Thr Ser Leu Arg Val Cys Ser Ser Cys Pro Val Gly Thr Phe
 40                  45                  50                  55

acc agg cat gag aat ggc ata gag aaa tgc cat gac tgt agt cag cca   336
Thr Arg His Glu Asn Gly Ile Glu Lys Cys His Asp Cys Ser Gln Pro
                60                  65                  70

tgc cca tgg cca atg att gag aaa tta cct tgt gct gcc ttg act gac   384
Cys Pro Trp Pro Met Ile Glu Lys Leu Pro Cys Ala Ala Leu Thr Asp
            75                  80                  85

cga gaa tgc act tgc cca cct ggc atg ttc cag tct aac gct acc tgt   432
Arg Glu Cys Thr Cys Pro Pro Gly Met Phe Gln Ser Asn Ala Thr Cys
        90                  95                  100

gcc ccc cat acg gtg tgt cct gtg ggt tgg ggt gtg cgg aag aaa ggg   480
Ala Pro His Thr Val Cys Pro Val Gly Trp Gly Val Arg Lys Lys Gly
    105                 110                 115

aca gag act gag gat gtg cgg tgt aag cag tgt gct cgg ggt acc ttc   528
Thr Glu Thr Glu Asp Val Arg Cys Lys Gln Cys Ala Arg Gly Thr Phe
120                 125                 130                 135

tca gat gtg cct tct agt gtg atg aaa tgc aaa gca tac aca gac tgt   576
Ser Asp Val Pro Ser Ser Val Met Lys Cys Lys Ala Tyr Thr Asp Cys
                140                 145                 150

ctg agt cag aac ctg gtg gtg atc aag ccg ggg acc aag gag aca gac   624
Leu Ser Gln Asn Leu Val Val Ile Lys Pro Gly Thr Lys Glu Thr Asp
            155                 160                 165

aac gtc tgt ggc aca ctc ccg tcc ttc tcc agc tcc acc tca cct tcc   672
Asn Val Cys Gly Thr Leu Pro Ser Phe Ser Ser Ser Thr Ser Pro Ser
        170                 175                 180

cct ggc aca gcc atc ttt cca cgc cct gag cac atg gaa acc cat gaa   720
Pro Gly Thr Ala Ile Phe Pro Arg Pro Glu His Met Glu Thr His Glu
    185                 190                 195

gtc cct tcc tcc act tat gtt ccc aaa ggc atg aac tca aca gaa tcc   768
Val Pro Ser Ser Thr Tyr Val Pro Lys Gly Met Asn Ser Thr Glu Ser
200                 205                 210                 215
```

```
aac tct tct gcc tct gtt aga cca aag gta ctg agt agc atc cag gaa   816
Asn Ser Ser Ala Ser Val Arg Pro Lys Val Leu Ser Ser Ile Gln Glu
                220                 225                 230

ggg aca gtc cct gac aac aca agc tca gca agg ggg aag gaa gac gtg   864
Gly Thr Val Pro Asp Asn Thr Ser Ser Ala Arg Gly Lys Glu Asp Val
            235                 240                 245

aac aag acc ctc cca aac ctt cag gta gtc aac cac cag caa ggc ccc   912
Asn Lys Thr Leu Pro Asn Leu Gln Val Val Asn His Gln Gln Gly Pro
        250                 255                 260

cac cac aga cac atc ctg aag ctg ctg ccg tcc atg gag gcc act ggg   960
His His Arg His Ile Leu Lys Leu Leu Pro Ser Met Glu Ala Thr Gly
    265                 270                 275

ggc gag aag tcc agc acg ccc atc aag ggc ccc aag agg gga cat cct  1008
Gly Glu Lys Ser Ser Thr Pro Ile Lys Gly Pro Lys Arg Gly His Pro
280                 285                 290                 295

aga cag aac cta cac aag cat ttt gac atc aat gag cat ttg ccc tgg  1056
Arg Gln Asn Leu His Lys His Phe Asp Ile Asn Glu His Leu Pro Trp
                300                 305                 310

atg att gtg ctt ttc ctg ctg ctg gtg ctt gtg gtg att gtg gtg tgc  1104
Met Ile Val Leu Phe Leu Leu Leu Val Leu Val Val Ile Val Val Cys
            315                 320                 325

agt atc cgg aaa agc tcg agg act ctg aaa aag ggg ccc cgg cag gat  1152
Ser Ile Arg Lys Ser Ser Arg Thr Leu Lys Lys Gly Pro Arg Gln Asp
        330                 335                 340

ccc agt gcc att gtg gaa aag gca ggg ctg aag aaa tcc atg act cca  1200
Pro Ser Ala Ile Val Glu Lys Ala Gly Leu Lys Lys Ser Met Thr Pro
    345                 350                 355

acc cag aac cgg gag aaa tgg atc tac tac tgc aat ggc cat gga ccc  1248
Thr Gln Asn Arg Glu Lys Trp Ile Tyr Tyr Cys Asn Gly His Gly Pro
360                 365                 370                 375

cat gat gag gag tgg ggg ttg atg gag aga cat att caa gat att tat  1296
His Asp Glu Glu Trp Gly Leu Met Glu Arg His Ile Gln Asp Ile Tyr
                380                 385                 390

att caa aga agc aat caa gat tca gaa aga tgg ggt tgataatttt       1342
Ile Gln Arg Ser Asn Gln Asp Ser Glu Arg Trp Gly
            395                 400

tacttcaccc tgggaggcag catagtgcag tgaaaggtat cgatatcctg aagcttgtag 1402

cagcccaagt gggaagccag tggaaagata tctatcagtt tctttgcaat gccagtgaga 1462

gggaggttgc tg                                                    1474


<210> 8
<211> 444
<212> PRT
<213> primate
```

<400> 8

```
Met Gly Thr Ser Pro Ser Ser Ser Thr Ala Leu Ala Ser Cys Ser Arg
-40                 -35                 -30

Ile Ala Arg Arg Ala Thr Ala Thr Met Ile Ala Gly Ser Leu Leu Leu
-25                 -20                 -15                 -10

Leu Gly Phe Leu Ser Thr Thr Thr Ala Gln Pro Glu Gln Lys Ala Ser
                -5                  -1  1                   5

Asn Leu Ile Gly Thr Tyr Arg His Val Asp Arg Ala Thr Gly Gln Val
            10                  15                  20

Leu Thr Cys Asp Lys Cys Pro Ala Gly Thr Tyr Val Ser Glu His Cys
        25                  30                  35

Thr Asn Thr Ser Leu Arg Val Cys Ser Ser Cys Pro Val Gly Thr Phe
    40                  45                  50                  55

Thr Arg His Glu Asn Gly Ile Glu Lys Cys His Asp Cys Ser Gln Pro
                60                  65                  70

Cys Pro Trp Pro Met Ile Glu Lys Leu Pro Cys Ala Ala Leu Thr Asp
            75                  80                  85

Arg Glu Cys Thr Cys Pro Pro Gly Met Phe Gln Ser Asn Ala Thr Cys
        90                  95                  100

Ala Pro His Thr Val Cys Pro Val Gly Trp Gly Val Arg Lys Lys Gly
    105                 110                 115

Thr Glu Thr Glu Asp Val Arg Cys Lys Gln Cys Ala Arg Gly Thr Phe
120                 125                 130                 135

Ser Asp Val Pro Ser Ser Val Met Lys Cys Lys Ala Tyr Thr Asp Cys
                140                 145                 150

Leu Ser Gln Asn Leu Val Val Ile Lys Pro Gly Thr Lys Glu Thr Asp
            155                 160                 165

Asn Val Cys Gly Thr Leu Pro Ser Phe Ser Ser Ser Thr Ser Pro Ser
        170                 175                 180

Pro Gly Thr Ala Ile Phe Pro Arg Pro Glu His Met Glu Thr His Glu
    185                 190                 195

Val Pro Ser Ser Thr Tyr Val Pro Lys Gly Met Asn Ser Thr Glu Ser
200                 205                 210                 215

Asn Ser Ser Ala Ser Val Arg Pro Lys Val Leu Ser Ser Ile Gln Glu
                220                 225                 230

Gly Thr Val Pro Asp Asn Thr Ser Ser Ala Arg Gly Lys Glu Asp Val
            235                 240                 245

Asn Lys Thr Leu Pro Asn Leu Gln Val Val Asn His Gln Gln Gly Pro
        250                 255                 260

His His Arg His Ile Leu Lys Leu Leu Pro Ser Met Glu Ala Thr Gly
    265                 270                 275
```

Sub A2

Gly Glu Lys Ser Ser Thr Pro Ile Lys Gly Pro Lys Arg Gly His Pro
280 285 290 295

Arg Gln Asn Leu His Lys His Phe Asp Ile Asn Glu His Leu Pro Trp
300 305 310

Met Ile Val Leu Phe Leu Leu Leu Val Leu Val Val Ile Val Val Cys
315 320 325

Ser Ile Arg Lys Ser Ser Arg Thr Leu Lys Lys Gly Pro Arg Gln Asp
330 335 340

Pro Ser Ala Ile Val Glu Lys Ala Gly Leu Lys Lys Ser Met Thr Pro
345 350 355

Thr Gln Asn Arg Glu Lys Trp Ile Tyr Tyr Cys Asn Gly His Gly Pro
360 365 370 375

His Asp Glu Glu Trp Gly Leu Met Glu Arg His Ile Gln Asp Ile Tyr
380 385 390

Ile Gln Arg Ser Asn Gln Asp Ser Glu Arg Trp Gly
395 400

<210> 9
<211> 227
<212> PRT
<213> rodent

<400> 9
Met Ala Pro Ala Ala Leu Trp Val Ala Leu Val Phe Glu Leu Gln Leu
1 5 10 15

Trp Ala Thr Gly His Thr Val Pro Ala Gln Val Val Leu Thr Pro Tyr
20 25 30

Lys Pro Glu Pro Gly Tyr Glu Cys Gln Ile Ser Gln Glu Tyr Tyr Asp
35 40 45

Arg Lys Ala Gln Met Cys Cys Ala Lys Cys Pro Pro Gly Gln Tyr Val
50 55 60

Lys His Phe Cys Asn Lys Thr Ser Asp Thr Val Cys Ala Asp Cys Glu
65 70 75 80

Ala Ser Met Tyr Thr Gln Val Trp Asn Gln Phe Arg Thr Cys Leu Ser
85 90 95

Cys Ser Ser Ser Cys Thr Thr Asp Gln Val Glu Ile Arg Ala Cys Thr
100 105 110

Lys Gln Gln Asn Arg Val Cys Ala Cys Glu Ala Gly Arg Tyr Cys Ala
115 120 125

Leu Lys Thr His Ser Gly Ser Cys Arg Gln Cys Met Arg Leu Ser Lys
130 135 140

Cys Gly Pro Gly Phe Gly Val Ala Ser Ser Arg Ala Pro Asn Gly Asn

Sub A2

145 150 155 160

Val Leu Cys Lys Ala Cys Ala Pro Gly Thr Phe Ser Asp Thr Thr Ser
165 170 175

Ser Thr Asp Val Cys Arg Pro His Arg Ile Cys Ser Ile Leu Ala Ile
180 185 190

Pro Gly Asn Ala Ser Thr Asp Ala Val Cys Ala Pro Glu Ser Pro Thr
195 200 205

Leu Ser Ala Ile Pro Arg Thr Leu Tyr Val Ser Gln Pro Glu Pro Thr
210 215 220

Arg Ser Gln
225

<210> 10
<211> 225
<212> PRT
<213> primate

<400> 10
Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu
1 5 10 15

Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
20 25 30

Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
35 40 45

Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
50 55 60

Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65 70 75 80

Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
85 90 95

Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
100 105 110

Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
115 120 125

Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
130 135 140

Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145 150 155 160

Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
165 170 175

Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
180 185 190

Sub A7

Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
195 200 205

Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
210 215 220

Gln
225

<210> 11
<211> 187
<212> PRT
<213> primate

<400> 11
Met Asn Lys Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile
1 5 10 15

Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
20 25 30

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr
35 40 45

Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro
50 55 60

Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
65 70 75 80

Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu
85 90 95

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr
100 105 110

Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe
115 120 125

Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg
130 135 140

Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys
145 150 155 160

Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys
165 170 175

Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly
180 185

<210> 12
<211> 636
<212> DNA
<213> rodent

<220>
<221> CDS

<222> (104)..(553)

<220>
<221> mat_peptide
<222> (191)..(553)

<400> 12
ggcacgaggg cgtttggcgc ggaagtgcta ccaagctgcg gaaagcgtga gtctggagca 60

cagcactggc gagtagcagg aataaacacg tttggtgaga gcc atg gca ctc aag 115
Met Ala Leu Lys

gtc cta cct cta cac agg acg gtg ctc ttc gct gcc att ctc ttc cta 163
Val Leu Pro Leu His Arg Thr Val Leu Phe Ala Ala Ile Leu Phe Leu
-25 -20 -15 -10

ctc cac ctg gca tgt aaa gtg agt tgc gaa acc gga gat tgc agg cag 211
Leu His Leu Ala Cys Lys Val Ser Cys Glu Thr Gly Asp Cys Arg Gln
-5 -1 1 5

cag gaa ttc aag gat cga tct gga aac tgt gtc ctc tgc aaa cag tgc 259
Gln Glu Phe Lys Asp Arg Ser Gly Asn Cys Val Leu Cys Lys Gln Cys
10 15 20

gga cct ggc atg gag ttg tcc aag gaa tgt ggc ttc ggc tat ggg gag 307
Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe Gly Tyr Gly Glu
25 30 35

gat gca cag tgt gtg ccc tgc agg ccg cac cgg ttc aag gaa gac tgg 355
Asp Ala Gln Cys Val Pro Cys Arg Pro His Arg Phe Lys Glu Asp Trp
40 45 50 55

ggt ttc cag aag tgt aag cca tgt gcg gac tgt gcg ctg gtg aac cgc 403
Gly Phe Gln Lys Cys Lys Pro Cys Ala Asp Cys Ala Leu Val Asn Arg
60 65 70

ttt cag agg gcc aac tgc tca cac acc agt gat gct gtc tgc ggg gac 451
Phe Gln Arg Ala Asn Cys Ser His Thr Ser Asp Ala Val Cys Gly Asp
75 80 85

tgc ctg cca gga ttt tac cgg aag acc aaa ctg gtt ggt ttt caa gac 499
Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val Gly Phe Gln Asp
90 95 100

atg gag tgt gtg ccc tgc gga gac cca cct cct ccc tac gaa cca cac 547
Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Pro Tyr Glu Pro His
105 110 115

tgt gag tgatgtgcca agtggcagca gacctttaaa aaaaaaagaa aaaaaaacaa 603
Cys Glu
120

acaaaaacaa aaaaaaaaaa aaaaaaaaaa aaa 636

<210> 13
<211> 150
<212> PRT
<213> rodent

Sub A2

<400> 13
Met Ala Leu Lys Val Leu Pro Leu His Arg Thr Val Leu Phe Ala Ala
-25 -20 -15

Ile Leu Phe Leu Leu His Leu Ala Cys Lys Val Ser Cys Glu Thr Gly
-10 -5 -1 1

Asp Cys Arg Gln Gln Glu Phe Lys Asp Arg Ser Gly Asn Cys Val Leu
5 10 15

Cys Lys Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe
20 25 30 35

Gly Tyr Gly Glu Asp Ala Gln Cys Val Pro Cys Arg Pro His Arg Phe
40 45 50

Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Ala Asp Cys Ala
55 60 65

Leu Val Asn Arg Phe Gln Arg Ala Asn Cys Ser His Thr Ser Asp Ala
70 75 80

Val Cys Gly Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val
85 90 95

Gly Phe Gln Asp Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Pro
100 105 110 115

Tyr Glu Pro His Cys Glu
120

<210> 14
<211> 474
<212> DNA
<213> primate

<220>
<221> CDS
<222> (78)..(473)

<220>
<221> misc_feature
<222> (308)
<223> N at 308, 315, 333, 412, 431, 436, 444, and 473 may be A, C, G, or T; translated amino acid depends on genetic code

<400> 14
cgcgctgagg tggatttgta ccggagtccc atttgggagc aagagccatc tactcgtccg 60

ttaccggcct tcccacc atg gat tgc caa gaa aat gag tac tgg gac caa 110
Met Asp Cys Gln Glu Asn Glu Tyr Trp Asp Gln
1 5 10

tgg gga cgg tgt gtc acc tgc caa cgg tgt ggt cct gga cag gag cta 158
Trp Gly Arg Cys Val Thr Cys Gln Arg Cys Gly Pro Gly Gln Glu Leu
15 20 25

tcc aag gat tgt ggt tat gga gag ggt gga gat gcc tac tgc aca gcc 206

```
Ser Lys Asp Cys Gly Tyr Gly Glu Gly Gly Asp Ala Tyr Cys Thr Ala
          30                  35                  40

tgc cct cct cgc agt aca aaa gca gct ggg gcc acc aca aat gtc aga   254
Cys Pro Pro Arg Ser Thr Lys Ala Ala Gly Ala Thr Thr Asn Val Arg
     45                  50                  55

gtt gca tca cct gtg ctg tca tca atc gtg ttc aga agg ttc aac tgc   302
Val Ala Ser Pro Val Leu Ser Ser Ile Val Phe Arg Arg Phe Asn Cys
 60                  65                  70                  75

aca gtn acc tct nat gct gtc tgt ggg gga ngg ttt gcc caa gtt tct   350
Thr Xaa Thr Ser Xaa Ala Val Cys Gly Gly Xaa Phe Ala Gln Val Ser
                 80                  85                  90

aac cga aag aca cgc cat tgg aag gct gcc agg acc aag gat ggc atc   398
Asn Arg Lys Thr Arg His Trp Lys Ala Ala Arg Thr Lys Asp Gly Ile
            95                  100                 105

ccg tgg cac aaa gnc aga ccc cca act tct gan ggt tnc aaa gtg nct   446
Pro Trp His Lys Xaa Arg Pro Pro Thr Ser Xaa Gly Xaa Lys Val Xaa
        110                 115                 120

ttc caa ttg gag ctt aat ggg agg can a                            474
Phe Gln Leu Glu Leu Asn Gly Arg Xaa
    125                 130


<210> 15
<211> 132
<212> PRT
<213> primate

<400> 15
Met Asp Cys Gln Glu Asn Glu Tyr Trp Asp Gln Trp Gly Arg Cys Val
  1               5                  10                  15

Thr Cys Gln Arg Cys Gly Pro Gly Gln Glu Leu Ser Lys Asp Cys Gly
             20                  25                  30

Tyr Gly Glu Gly Gly Asp Ala Tyr Cys Thr Ala Cys Pro Pro Arg Ser
         35                  40                  45

Thr Lys Ala Ala Gly Ala Thr Thr Asn Val Arg Val Ala Ser Pro Val
     50                  55                  60

Leu Ser Ser Ile Val Phe Arg Arg Phe Asn Cys Thr Xaa Thr Ser Xaa
 65                  70                  75                  80

Ala Val Cys Gly Gly Xaa Phe Ala Gln Val Ser Asn Arg Lys Thr Arg
                 85                  90                  95

His Trp Lys Ala Ala Arg Thr Lys Asp Gly Ile Pro Trp His Lys Xaa
            100                 105                 110

Arg Pro Pro Thr Ser Xaa Gly Xaa Lys Val Xaa Phe Gln Leu Glu Leu
        115                 120                 125

Asn Gly Arg Xaa
    130
```

Sub A2

<210> 16
<211> 546
<212> DNA
<213> primate

<220>
<221> CDS
<222> (78)..(308)

<220>
<221> misc_feature
<222> (317)
<223> N at 317, 340, 351, 389, 398, 428, 429, 433, 452, 468, 483, 534, and 541 may be A, C, G, or T

<400> 16
cgcgctgagg tggatttgta ccggagtccc atttgggagc aagagccatc tactcgtccg 60

ttaccggcct tcccacc atg gat tgc caa gaa aat gag tac tgg gac caa 110
Met Asp Cys Gln Glu Asn Glu Tyr Trp Asp Gln
1 5 10

tgg gga cgg tgt gtc acc tgc caa cgg tgt ggt cct gga cag gag cta 158
Trp Gly Arg Cys Val Thr Cys Gln Arg Cys Gly Pro Gly Gln Glu Leu
15 20 25

tcc aag gat tgt ggt tat gga gag ggt gga gat gcc tac tgc aca gcc 206
Ser Lys Asp Cys Gly Tyr Gly Glu Gly Gly Asp Ala Tyr Cys Thr Ala
30 35 40

tgc cct cct cgc agg tac aaa agc agc tgg ggc cac cac aaa tgt cag 254
Cys Pro Pro Arg Arg Tyr Lys Ser Ser Trp Gly His His Lys Cys Gln
45 50 55

agt tgc atc acc tgt gct gtc atc aat cgt gtt cag aag gtc caa ctg 302
Ser Cys Ile Thr Cys Ala Val Ile Asn Arg Val Gln Lys Val Gln Leu
60 65 70 75

cac agc taacctctna tgctgtctgt ggggatgttt gncccaagtt ctnaccgaaa 358
His Ser

agacacgcca tgggaaggct ggcaggacca ngaatggccn tcccgtggca gaaagccaga 418

ccccccaacn nctgnaggtt ccaatgtggc cttnccattt ggaagcttan tgggaaggca 478

gatgncaacc caaagtggcc ccttcaggga ggccaaaatt tgttggcaat gggtgnagca 538

gcntgcca 546

<210> 17
<211> 77
<212> PRT
<213> primate

<400> 17
Met Asp Cys Gln Glu Asn Glu Tyr Trp Asp Gln Trp Gly Arg Cys Val

```
  1               5                  10                  15

Thr Cys Gln Arg Cys Gly Pro Gly Gln Glu Leu Ser Lys Asp Cys Gly
            20                  25                  30

Tyr Gly Glu Gly Gly Asp Ala Tyr Cys Thr Ala Cys Pro Pro Arg Arg
        35                  40                  45

Tyr Lys Ser Ser Trp Gly His His Lys Cys Gln Ser Cys Ile Thr Cys
    50                  55                  60

Ala Val Ile Asn Arg Val Gln Lys Val Gln Leu His Ser
65                  70                  75
```

<210> 18
<211> 932
<212> DNA
<213> primate

<220>
<221> CDS
<222> (78)..(770)

<220>
<221> misc_feature
<222> (782)
<223> N; may be A, C, G, or T

<400> 18
cgcgctgagg tggatttgta ccggagtccc atttgggagc aagagccatc tactcgtccg 60

```
ttaccggcct tcccacc atg gat tgc caa gaa aat gag tac tgg gac caa    110
                    Met Asp Cys Gln Glu Asn Glu Tyr Trp Asp Gln
                      1               5                  10

tgg gga cgg tgt gtc acc tgc caa cgg tgt ggt cct gga cag gag cta   158
Trp Gly Arg Cys Val Thr Cys Gln Arg Cys Gly Pro Gly Gln Glu Leu
             15                  20                  25

tcc aag gat tgt ggt tat gga gag ggt gga gat gcc tac tgc aca gcc   206
Ser Lys Asp Cys Gly Tyr Gly Glu Gly Gly Asp Ala Tyr Cys Thr Ala
         30                  35                  40

tgc cct cct cgc agg tac aaa agc agc tgg ggc cac cac aaa tgt cag   254
Cys Pro Pro Arg Arg Tyr Lys Ser Ser Trp Gly His His Lys Cys Gln
     45                  50                  55

agt tgc atc acc tgt gct gtc atc aat cgt gtt cag aag gtc aac tgc   302
Ser Cys Ile Thr Cys Ala Val Ile Asn Arg Val Gln Lys Val Asn Cys
 60                  65                  70                  75

aca gct acc tct aat gct gtc tgt ggg gac tgt ttg ccc agg ttc tac   350
Thr Ala Thr Ser Asn Ala Val Cys Gly Asp Cys Leu Pro Arg Phe Tyr
                 80                  85                  90

cga aag aca cgc att gga ggc ctg cag gac caa gag tgc atc ccg tgc   398
Arg Lys Thr Arg Ile Gly Gly Leu Gln Asp Gln Glu Cys Ile Pro Cys
             95                  100                 105
```

```
acg aag cag acc ccc acc tct gag gtt caa tgt gcc ttc cag ttg agc   446
Thr Lys Gln Thr Pro Thr Ser Glu Val Gln Cys Ala Phe Gln Leu Ser
        110                 115                 120

tta gtg gag gca gat gca ccc aca gtg ccc cct cag gag gcc aca ctt   494
Leu Val Glu Ala Asp Ala Pro Thr Val Pro Pro Gln Glu Ala Thr Leu
    125                 130                 135

gtt gca ctg gtg agc agc ctg cta gtg gtg ttt acc ctg gcc ttc ctg   542
Val Ala Leu Val Ser Ser Leu Leu Val Val Phe Thr Leu Ala Phe Leu
140                 145                 150                 155

ggg ctc ttc ttc ctc tac tgc aag cag ttc ttc aac aga cat tgc cag   590
Gly Leu Phe Phe Leu Tyr Cys Lys Gln Phe Phe Asn Arg His Cys Gln
                160                 165                 170

cgt gga ggt ttg ctg cag ttt gag gct gat aaa aca gca aag gag gaa   638
Arg Gly Gly Leu Leu Gln Phe Glu Ala Asp Lys Thr Ala Lys Glu Glu
            175                 180                 185

tct ctc ttc ccc gtg cca ccc agc aag gag acc agt gct gag tcc caa   686
Ser Leu Phe Pro Val Pro Pro Ser Lys Glu Thr Ser Ala Glu Ser Gln
        190                 195                 200

gtc tct tgg gcc cct ggc agc ctt gcc cag ttg ttc tct ctg gac tct   734
Val Ser Trp Ala Pro Gly Ser Leu Ala Gln Leu Phe Ser Leu Asp Ser
    205                 210                 215

gtt cct ata cca caa cag cag cag ggg cct gaa atg tgatgtccac        780
Val Pro Ile Pro Gln Gln Gln Gln Gly Pro Glu Met
220                 225                 230

angagctaat accctacaga tggggcatat cctatcccat cccaccagag gattgattct 840

ccatttcaca aggactgatc tggagcattt cttgcttccc tgttgtagtc tggggagcca 900

gattccacat tcatgggact accagacatg tt                              932
```

<210> 19
<211> 231
<212> PRT
<213> primate

<400> 19

```
Met Asp Cys Gln Glu Asn Glu Tyr Trp Asp Gln Trp Gly Arg Cys Val
  1               5                  10                  15

Thr Cys Gln Arg Cys Gly Pro Gly Gln Glu Leu Ser Lys Asp Cys Gly
            20                  25                  30

Tyr Gly Glu Gly Gly Asp Ala Tyr Cys Thr Ala Cys Pro Pro Arg Arg
        35                  40                  45

Tyr Lys Ser Ser Trp Gly His His Lys Cys Gln Ser Cys Ile Thr Cys
    50                  55                  60

Ala Val Ile Asn Arg Val Gln Lys Val Asn Cys Thr Ala Thr Ser Asn
65                  70                  75                  80
```

Ala Val Cys Gly Asp Cys Leu Pro Arg Phe Tyr Arg Lys Thr Arg Ile
85 90 95

Gly Gly Leu Gln Asp Gln Glu Cys Ile Pro Cys Thr Lys Gln Thr Pro
100 105 110

Thr Ser Glu Val Gln Cys Ala Phe Gln Leu Ser Leu Val Glu Ala Asp
115 120 125

Ala Pro Thr Val Pro Pro Gln Glu Ala Thr Leu Val Ala Leu Val Ser
130 135 140

Ser Leu Leu Val Val Phe Thr Leu Ala Phe Leu Gly Leu Phe Phe Leu
145 150 155 160

Tyr Cys Lys Gln Phe Phe Asn Arg His Cys Gln Arg Gly Gly Leu Leu
165 170 175

Gln Phe Glu Ala Asp Lys Thr Ala Lys Glu Glu Ser Leu Phe Pro Val
180 185 190

Pro Pro Ser Lys Glu Thr Ser Ala Glu Ser Gln Val Ser Trp Ala Pro
195 200 205

Gly Ser Leu Ala Gln Leu Phe Ser Leu Asp Ser Val Pro Ile Pro Gln
210 215 220

Gln Gln Gln Gly Pro Glu Met
225 230